SEQUENCE LISTING

<110> Piddington, Christopher S.
      Petrie, Charles
      Shoemaker, Kimberly E.
      Bishop, Paul D.

<120> ZACE2: A HUMAN METALLOENZYME

<130> 99-24C1

<150> 60/133,952
<151> 1999-05-13

<150> 60/151,181
<151> 1999-08-27

<150> 09/563,516
<151> 2000-05-03

<160> 11

<170> FastSEQ for Windows Version 3.0

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<212> DNA
<213> Homo sapiens

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<222> (35)...(2449)

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ctt ctc agc ctt gtt gct gta act gct gct cag tcc acc att gag gaa   103
Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu
        10   15   20

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cag gcc aag aca ttt ttg gac aag ttt aac cac gaa gcc gaa gac ctg        151
Gln Ala Lys Thr Phe Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu
        25              30                  35

ttc tat caa agt tca ctt gct tct tgg aat tat aac acc aat att act        199
Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr
40                  45                  50                  55

gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc        247
Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala
                60                  65                  70

ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa        295
Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu
                75                  80                  85

att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt cag caa aat        343
Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn
            90                  95                  100

ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg aac aca att        391
Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile
    105                 110                 115

cta aat aca atg agc acc atc tac agt act gga aaa gtt tgt aac cca        439
Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro
120                 125                 130                 135

gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata        487
Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile
                140                 145                 150

atg gca aac agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc        535
Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser
                155                 160                 165

tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat        583
Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr
        170                 175                 180

gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat gag gac tat        631
Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr
        185                 190                 195
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ggg gat tat tgg aga gga gac tat gaa gta aat ggg gta gat ggc tat       679
Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr
200             205             210             215

gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa       727
Asp Tyr Ser Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu
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gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag       775
Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys
                235             240             245

ttg atg aat gcc tat cct tcc tat atc agt cca att gga tgc ctc cct       823
Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro
            250             255             260

gct cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac       871
Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr
        265             270             275

tct ttg aca gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat       919
Ser Leu Thr Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp
280             285             290             295

gca atg gtg gac cag gcc tgg gat gca cag aga ata ttc aag gag gcc       967
Ala Met Val Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala
                300             305             310

gag aag ttc ttt gta tct gtt ggt ctt cct aat atg act caa gga ttc      1015
Glu Lys Phe Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe
                315             320             325

tgg gaa aat tcc atg cta acg gac cca gga aat gtt cag aaa gca gtc      1063
Trp Glu Asn Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val
                330             335             340

tgc cat ccc aca gct tgg gac ctg ggg aag ggc gac ttc agg atc ctt      1111
Cys His Pro Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu
        345             350             355

atg tgc aca aag gtg aca atg gac gac ttc ctg aca gct cat cat gag      1159
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Met Cys Thr Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu
360             365             370             375

atg ggg cat atc cag tat gat atg gca tat gct gca caa cct ttt ctg    1207
Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu
            380             385             390

cta aga aat gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc    1255
Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile
            395             400             405

atg tca ctt tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt    1303
Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu
        410             415             420

ctg tca ccc gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg    1351
Leu Ser Pro Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu
        425             430             435

ctc aaa caa gca ctc acg att gtt ggg act ctg cca ttt act tac atg    1399
Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met
440             445             450             455

tta gag aag tgg agg tgg atg gtc ttt aaa ggg gaa att ccc aaa gac    1447
Leu Glu Lys Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp
            460             465             470

cag tgg atg aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg    1495
Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val
            475             480             485

gtg gaa cct gtg ccc cat gat gaa aca tac tgt gac ccc gca tct ctg    1543
Val Glu Pro Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu
            490             495             500

ttc cat gtt tct aat gat tac tca ttc att cga tat tac aca agg acc    1591
Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr
        505             510             515

ctt tac caa ttc cag ttt caa gaa gca ctt tgt caa gca gct aaa cat    1639
Leu Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His
520             525             530             535
```

```
gaa ggc cct ctg cac aaa tgt gac atc tca aac tct aca gaa gct gga      1687
Glu Gly Pro Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly
                540             545             550

cag aaa ctg ttc aat atg ctg agg ctt gga aaa tca gaa ccc tgg acc      1735
Gln Lys Leu Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr
                555             560             565

cta gca ttg gaa aat gtt gta gga gca aag aac atg aat gta agg cca      1783
Leu Ala Leu Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro
                570             575             580

ctg ctc aac tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac      1831
Leu Leu Asn Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn
        585             590             595

aag aat tct ttt gtg gga tgg agt acc gac tgg agt cca tat gca gac      1879

Lys Asn Ser Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp
600             605             610             615

caa agc atc aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa      1927
Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys
                620             625             630

gca tat gaa tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt      1975
Ala Tyr Glu Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val
                635             640             645

gca tat gct atg agg cag tac ttt tta aaa gta aaa aat cag atg att      2023
Ala Tyr Ala Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile
                650             655             660

ctt ttt ggg gag gag gat gtg cga gtg gct aat ttg aaa cca aga atc      2071
Leu Phe Gly Glu Glu Asp Val Arg Val Ala Asn Leu Lys Pro Arg Ile
                665             670             675

tcc ttt aat ttc ttt gtc act gca cct aaa aat gtg tct gat atc att      2119
Ser Phe Asn Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile
680             685             690             695

cct aga act gaa gtt gaa aag gcc atc agg atg tcc cgg agc cgt atc      2167
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```
Pro Arg Thr Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile
            700               705               710
```

```
aat gat gct ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata    2215
Asn Asp Ala Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile
            715               720               725
```

```
cag cca aca ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg    2263
Gln Pro Thr Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu
            730               735               740
```

```
att gtt ttt gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc    2311
Ile Val Phe Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile
            745               750               755
```

```
ctg atc ttc act ggg atc aga gat cgg aag aag aaa aat aaa gca aga    2359
Leu Ile Phe Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg
760               765               770               775
```

```
agt gga gaa aat cct tat gcc tcc atc gat att agc aaa gga gaa aat    2407
Ser Gly Glu Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn
                780               785               790
```

```
aat cca gga ttc caa aac act gat gat gtt cag acc tcc ttt           2449
Asn Pro Gly Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
            795               800               805
```

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tagaaaaatc tatgtttttc ctcttgaggt gattttgttg tatgtaaatg ttaatttcat    2509
ggtatagaaa atataagatg ataaagatat cattaaatgt caaaactatg actctgttca    2569
gaaaaaaaat tgtccaaaga caacatggcc aaggagagag catcttcatt gacattgctt    2629
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gctgcaagga ttgagaatgg catgcattag ctcactttca tttaatccat tgtcaaggat    2929
gacatgcttt cttcacagta actcagttca agtactatgg tgatttgcct acagtgatgt    2989
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aggtagagga cattgctttt tcacttccaa ggtgcttgat caacatctcc ctgacaacac    3109
aaaactagag ccaggggcct ccgtgaactc ccagagcatg cctgatagaa actcatttct    3169
actgttctct aactgtggag tgaatggaaa ttccaactgt atgttcaccc tctgaagtgg    3229
gtacccagtc tcttaaatct tttgtatttg ctcacagtgt ttgagcagtg ctgagcacaa    3289
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<212> PRT
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Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
        35                  40                  45
Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
        50                  55                  60
Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
65                  70                  75                  80
Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln
                85                  90                  95
Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
            100                 105                 110
Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
            115                 120                 125
Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu
        130                 135                 140
Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu
145                 150                 155                 160
Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu
                165                 170                 175
Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
                180                 185                 190
Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
            195                 200                 205
Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu
        210                 215                 220
Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu
225                 230                 235                 240
His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile
                245                 250                 255
Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
            260                 265                 270
Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
            275                 280                 285
```

```
Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
    290                 295                 300
Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
305                 310                 315                 320
Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
            325                 330                 335
Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
            340                 345                 350
Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
            355                 360                 365
Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
    370                 375                 380
Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
385                 390                 395                 400
His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
            405                 410                 415
His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
            420                 425                 430
Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
        435                 440                 445
Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
    450                 455                 460
Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
465                 470                 475                 480
Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
            485                 490                 495
Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
            500                 505                 510
Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
            515                 520                 525
Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
    530                 535                 540
Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu
545                 550                 555                 560
Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
            565                 570                 575
Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
            580                 585                 590
Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
    595                 600                 605
Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
    610                 615                 620
```

```
Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
625                 630             635                 640
Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
            645             650             655
Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
            660             665             670
Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
        675             680             685
Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
        690             695             700
Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
705             710             715                 720
Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
            725             730             735
Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
            740             745             750
Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
            755             760             765
Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
        770             775             780
Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
785             790             795                 800
Val Gln Thr Ser Phe
                805
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<210> 3
<211> 2415
<212> DNA
<213> Artificial Sequence

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      sequence of SEQ ID NO:2.

<221> misc_feature
<222> (1)...(2415)
<223> n = A,T,C or G

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athgargarc argcnaarac nttyytngay aarttyaayc aygargcnga rgayytntty   120
taycarwsnw snytngcnws ntggaaytay aayacnaaya thacngarga raaygtncar   180
aayatgaaya aygcnggnga yaartggwsn gcnttyytna argarcarws nacnytngcn   240
```

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caratgtayc cnytncarga rathcaraay ytnacngtna arytncaryt ncargcnytn    300
carcaraayg gnwsnwsngt nytnwsngar gayaarwsna armgnytnaa yacnathytn    360
aayacnatgw snacnathta ywsnacnggn aargtntgya ayccngayaa yccncargar    420
tgyytnytny tngarccngg nytnaaygar athatggcna aywsnytnga ytayaaygar    480
mgnytntggg cntgggarws ntggmgnwsn gargtnggna arcarytnmg nccnytntay    540
gargartayg tngtnytnaa raaygaratg gcnmgngcna aycaytayga rgaytayggn    600
gaytaytggm gnggngayta ygargtnaay gggntngayg gntaygayta ywsnmgnggn    660
carytnathg argaygtnga rcayacntty gargaratha arccnytnta ygarcayytn    720
caygcntayg tnmgngcnaa rytnatgaay gcntayccnw sntayathws nccnathggn    780
tgyytnccng cncayytnyt nggngayatg tggggnmgnt tytggacnaa yytntaywsn    840
ytnacngtnc cnttyggnca raarccnaay athgaygtna cngaygcnat ggtngaycar    900
gcntgggayg cncarmgnat httyaargar gcngaraart tyttygtnws ngtnggnytn    960
ccnaayatga cncarggntt ytgggaraay wsnatgytna cngayccngg naaygtncar   1020
aargcngtnt gycayccnac ngcntgggay ytnggnaarg gngayttymg nathytnatg   1080
tgyacnaarg tnacnatgga ygayttyytn acngcncayc aygaratggg ncayathcar   1140
taygayatgg cntaygcngc ncarccntty ytnytnmgna ayggngcnaa ygarggntty   1200
caygargcng tnggngarat hatgwsnytn wsngcngcna cnccnaarca yytnaarwsn   1260
athggnytny tnwsnccnga yttycargar gayaaygara cngarathaa yttyytnytn   1320
aarcargcny tnacnathgt nggnacnytn ccnttyacnt ayatgytnga raartggmgn   1380
tggatggtnt tyaarggnga rathccnaar gaycartgga tgaaraartg gtgggaratg   1440
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gcnwsnytnt tycaygtnws naaygaytay wsnttyathm gntaytayac nmgnacnytn   1560
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aaywsnttyg tnggntggws nacngaytgg wsnccntayg cngaycarws nathaargtn   1860
mgnathwsny tnaarwsngc nytnggngay aargcntayg artggaayga yaaygaratg   1920
tayytnttym gnwsnwsngt ngcntaygcn atgmgncart ayttyytnaa rgtnaaraay   1980
caratgathy tnttyggnga rgargaygtn mgngtngcna ayytnaarcc nmgnathwsn   2040
ttyaayttyt tygtnacngc nccnaaraay gtnwsngaya thathccnmg nacngargtn   2100
garaargcna thmgnatgws nmgnwsnmgn athaaygayg cnttymgnyt naaygayaay   2160
wsnytngart tyytnggnat hcarccnacn ytnggnccnc cnaaycarcc nccngtnwsn   2220
athtggytna thgtnttygg ngtngtnatg gggntnathg tngtnggnat hgtnathytn   2280
athttyacng gnathmgnga ymgnaaraar aaraayaarg cnmgnwsngg ngaraayccn   2340
taygcnwsna thgayathws naarggngar aayaayccng gnttycaraa yacngaygay   2400
gtncaracnw sntty                                                    2415
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        <213> Artificial Sequence

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<212> DNA
<213> Mouse

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<221> CDS
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                                                 Met Ser Ser Ser
                                                   1

tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc   165
Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu
  5   10   15   20

acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gaa gct   213
Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
                    25   30   35

gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act   261
Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
                40   45   50

aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa   309
Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys
          55   60   65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca   357
Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser
  70   75   80

cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt   405

```
Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln Leu Gln Ala Leu
 85              90              95              100


cag caa agt ggg tct tca gca ctc tca gca gac aag aac aaa cag ttg      453
Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys Asn Lys Gln Leu
            105              110              115


aac aca att ctg aac acc atg agc acc att tac agt act gga aaa gtt      501
Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val
            120              125              130


tgc aac cca aag aac cca caa gaa tgc tta tta ctt gag cca gga ttg      549
Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu
            135              140              145


gat gaa ata atg gcg aca agc aca gac tac aac tct agg ctc tgg gca      597
Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser Arg Leu Trp Ala
    150              155              160


tgg gag ggc tgg agg gct gag gtt ggc aag cag ctg agg ccg ttg tat      645
Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr
165              170              175              180


gaa gag tat gtg gtc ctg aaa aac gag atg gca aga gca aac aat tat      693
Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn Asn Tyr
                185              190              195


aac gac tat ggg gat tat tgg aga ggg gac tat gaa gca gag gga gca      741
Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Ala Glu Gly Ala
            200              205              210


gat ggc tac aac tat aac cgt aac cag ttg att gaa gat gta gaa cgt      789
Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu Asp Val Glu Arg
            215              220              225


acc ttc gca gag atc aag cca ttg tat gag cat ctt cat gcc tat gtg      837
Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val
            230              235              240


agg agg aag ttg atg gat acc tac cct tcc tac atc agc ccc act gga      885
Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly
245              250              255              260
```

```
tgc ctc cct gcc cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca          933
Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr
            265                 270                 275


aat ctg tac cct ttg act gtt ccc ttt gca cag aaa cca aac ata gat          981
Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp
            280                 285                 290


gtt act gat gca atg atg aat cag ggc tgg gat gca gaa agg ata ttt          1029
Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe
            295                 300                 305


caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act          1077
Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr
            310                 315                 320


caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg          1125
Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg
325                 330                 335                 340


aaa gtt gtc tgc cac ccc aca gct tgg gat ctg gga cac gga gac ttc          1173
Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe
            345                 350                 355


aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc          1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala
                360                 365                 370


cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa          1269
His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln
            375                 380                 385


cct ttc ctg cta aga aac gga gcc aat gaa ggg ttc cat gaa gct gtt          1317
Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val
            390                 395                 400


gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc          1365
Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser
405                 410                 415                 420


att ggt ctt ctg cca tcc gat ttt caa gaa gat agc gaa aca gag ata          1413
Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile
            425                 430                 435
```

```
aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt    1461
Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe
            440                 445                 450

act tac atg tta gag aag tgg agg tgg atg gtc ttt cgg ggt gaa att    1509
Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile
            455                 460                 465

ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc    1557
Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile
    470                 475                 480

gtt ggt gtg gtg gag cct ctg cct cat gat gaa aca tac tgt gac cct    1605
Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr Tyr Cys Asp Pro
485                 490                 495                 500

gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac    1653
Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr
                505                 510                 515

aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca    1701
Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala
                520                 525                 530

gct aag tat aat ggt tct ctg cac aaa tgt gac atc tca aat tcc act    1749
Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr
            535                 540                 545

gaa gct ggg cag aag ttg ctc aag atg ctg agt ctt gga aat tca gag    1797
Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu
    550                 555                 560

ccc tgg acc aaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat    1845
Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp
565                 570                 575                 580

gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa    1893
Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys
                585                 590                 595

gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca    1941
```

```
Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro
        600             605             610

tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt      1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu
        615             620             625

gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga      2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg
        630             635             640

tca tct gtt gca tat gcc atg aga aag tat ttt tca ata atc aaa aac      2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser Ile Ile Lys Asn
645             650             655             660

cag aca gtt cct ttt cta gag gaa gat gta cga gtg agc gat ttg aaa      2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys
            665             670             675

cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct      2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser
            680             685             690

gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg      2229
Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg
            695             700             705

ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt      2277
Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe
        710             715             720

ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc      2325
Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr
725             730             735             740

ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc      2373
Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly
            745             750             755

atc atc atc ctg att gtc act ggg atc aaa ggt cga aag aag aaa aat      2421
```

```
Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn
        760                   765                   770
```

```
gaa aca aaa aga gaa gag aac cct tat gac tcg atg gac att gga aaa      2469
Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
        775                   780                   785
```

```
gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc      2517
Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
        790                   795                   800
```

```
ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac           2570
Phe
805
```

```
acaaaatatg agagtataca catgtcatta gctatcaaaa ctatgatctg ttcagtaaac    2630
gttgtcca                                                             2638
```

```
        <210> 6
        <211> 805
        <212> PRT
        <213> Mouse

        <400> 6
Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr
 1               5                   10                  15
Ala Gln Ser Leu Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe
            20                  25                  30
Asn Gln Glu Ala Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp
        35                  40                  45
Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu
    50                  55                  60
Ala Ala Ala Lys Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala
65                  70                  75                  80
Gln Ser Phe Ser Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln
                85                  90                  95
Leu Gln Ala Leu Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys
            100                 105                 110
Asn Lys Gln Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
        115                 120                 125
```

```
Thr Gly Lys Val Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu
    130             135             140
Glu Pro Gly Leu Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser
145             150             155             160
Arg Leu Trp Ala Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu
        165             170             175
Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
        180             185             190
Ala Asn Asn Tyr Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
        195             200             205
Ala Glu Gly Ala Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu
    210             215             220
Asp Val Glu Arg Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu
225             230             235             240
His Ala Tyr Val Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile
            245             250             255
Ser Pro Thr Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
        260             265             270
Arg Phe Trp Thr Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys
        275             280             285
Pro Asn Ile Asp Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala
    290             295             300
Glu Arg Ile Phe Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
305             310             315             320
Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
            325             330             335
Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
            340             345             350
His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
    355             360             365
Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
370             375             380
Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
385             390             395             400
His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
            405             410             415
His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
        420             425             430
Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
    435             440             445
Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
    450             455             460
```

```
Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
465             470             475                     480
Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr
                485             490                 495
Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
            500             505                 510
Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
        515                 520                 525
Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
        530                 535                 540
Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
545                 550                 555                 560
Gly Asn Ser Glu Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala
                565                 570                 575
Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
                580                 585                 590
Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
            595                 600                 605
Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
        610                 615                 620
Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
625                 630                 635                 640
Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser
                645                 650                 655
Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
                660                 665                 670
Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
            675                 680                 685
Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
    690                 695                 700
Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
705                 710                 715                 720
Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
                725                 730                 735
Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
                740                 745                 750
Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
            755                 760                 765
Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
    770                 775                 780
Asp Ile Gly Lys Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp
785                 790                 795                 800
```

Ala Gln Thr Ser Phe
                805

<210> 7
<211> 2415
<212> DNA
<213> Artificial Sequence

<220>
<223> This degenerate sequence encodes the amino acid
      sequence of SEQ ID NO:6.

<221> misc_feature
<222> (1)...(2415)
<223> n = A,T,C or G

<400> 7

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atgwsnwsnw snwsntggyt nytnytnwsn ytngtngcng tnacnacngc ncarwsnytn      60
acngargara aygcnaarac nttyytnaay aayttyaayc argargcnga rgayytnwsn     120
taycarwsnw snytngcnws ntggaaytay aayacnaaya thacngarga raaygcncar     180
aaratgwsng argcngcngc naartggwsn gcnttytayg argarcarws naaracngcn     240
carwsnttyw snytncarga rathcaracn ccnathatha armgncaryt ncargcnytn     300
carcarwsng gnwsnwsngc nytnwsngcn gayaaraaya arcarytnaa yacnathytn     360
aayacnatgw snacnathta ywsnacnggn aargtntgya ayccnaaraa yccncargar     420
tgyytnytny tngarccngg nytngaygar athatggcna cnwsnacnga ytayaaywsn     480
mgnytntggg cntgggargg ntggmgngcn gargtnggna arcarytnmg nccnytntay     540
gargartayg tngtnytnaa raaygaratg gcnmgngcna ayaaytayaa ygaytayggn     600
gaytaytggm gnggngayta ygargcngar ggngcngayg gntayaayta yaaymgnaay     660
carytnathg argaygtnga rmgnacntty gcngaratha arccnytnta ygarcayytn     720
caygcntayg tnmgnmgnaa rytnatggay acntayccnw sntayathws nccnacnggn     780
tgyytnccng cncayytnyt nggngayatg tggggnmgnt tytggacnaa yytntayccn     840
ytnacngtnc cnttygcnca raarccnaay athgaygtna cngaygcnat gatgaaycar     900
ggntgggayg cngarmgnat httycargar gcngaraart tyttygtnws ngtnggnytn     960
ccncayatga cncarggntt ytgggcnaay wsnatgytna cngarccngc ngayggnmgn    1020
aargtngtnt gycayccnac ngcntgggay ytnggncayg gngayttymg nathaaratg    1080
tgyacnaarg tnacnatgga yaayttyytn acngcncayc aygaratggg ncayathcar    1140
taygayatgg cntaygcnmg ncarccntty ytnytnmgna ayggngcnaa ygarggntty    1200
caygargcng tnggngarat hatgwsnytn wsngcngcna cnccnaarca yytnaarwsn    1260
athggnytny tnccnwsnga yttycargar gaywsngara cngarathaa yttyytnytn    1320
aarcargcny tnacnathgt nggnacnytn ccnttyacnt ayatgytnga raartggmgn    1380
tggatggtnt tymgnggnga rathccnaar garcartgga tgaaraartg gtgggaratg    1440
aarmgngara thgtnggngt ngtngarccn ytnccncayg aygaracnta ytgygayccn    1500
```

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gcnwsnytnt tycaygtnws naaygaytay wsnttyathm gntaytayac nmgnacnath    1560
taycarttyc arttycarga rgcnytntgy cargcngcna artayaaygg nwsnytncay    1620
aartgygaya thwsnaayws nacngargcn ggncaraary tnytnaarat gytnwsnytn    1680
ggnaaywsng arccntggac naargcnytn garaaygtng tnggngcnmg naayatggay    1740
gtnaarccny tnytnaayta yttycarccn ytnttygayt ggytnaarga rcaraaymgn    1800
aaywsnttyg tnggntggaa yacngartgg wsnccntayg cngaycarws nathaargtn    1860
mgnathwsny tnaarwsngc nytnggngcn aaygcntayg artggacnaa yaaygaratg    1920
ttyytnttym gnwsnwsngt ngcntaygcn atgmgnaart ayttywsnat hathaaraay    1980
caracngtnc cnttyytnga rgargaygtn mgngtnwsng ayytnaarcc nmgngtnwsn    2040
ttytayttyt tygtnacnws nccncaraay gtnwsngayg tnathccnmg nwsngargtn    2100
gargaygcna thmgnatgws nmgnggnmgn athaaygayg tnttyggnyt naaygayaay    2160
wsnytngart tyytnggnat hcayccnacn ytngarccnc cntaycarcc nccngtnacn    2220
athtggytna thathttygg ngtngtnatg gcnytngtng tngtnggnat hathathytn    2280
athgtnacng gnathaargg nmgnaaraar aaraaygara cnaarmgnga rgaraayccn    2340
taygaywsna tggayathgg naarggngar wsnaaygcng gnttycaraa ywsngaygay    2400
gcncaracnw sntty                                                    2415
```

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<210> 8
<211> 2638
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (106)...(2520)

<400> 8
agtgcccaac ccaagttcaa aggctgatga gagagaaaaa ctcatgaaga gattttactc     60
tagggaaagt tgctcagtgg atgggatctt ggcgcacggg gaaag atg tcc agc tcc    117
                                                   Met Ser Ser Ser
                                                     1


tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc    165
Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu
 5               10              15              20


acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gag gct    213
Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala
             25              30              35


gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act    261
Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr
             40              45              50
```

```
aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa        309
Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys
        55                      60                      65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca        357
Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser
        70                      75                      80

cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt        405
Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln Leu Gln Ala Leu
 85                      90                      95                 100

cag caa agt ggg tct tca gca ctc tca gca gac aag aac aaa cag ttg        453
Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys Asn Lys Gln Leu
                105                     110                     115

aac aca att ctg aac acc atg agc acc att tac agt act gga aaa gtt        501
Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val
                120                     125                     130

tgc aac cca agg aac cca caa gaa tgc tta tta ctt gag cca gga ttg        549
Cys Asn Pro Arg Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu
                135                     140                     145

gat gaa ata atg gcg aca agc aca gac tac aac tct agg ctc tgg gca        597
Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser Arg Leu Trp Ala
        150                     155                     160

tgg gag ggc tgg agg gct gag gtt ggc aag cag ctg agg ccg ttg tat        645
Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr
165                     170                     175                     180

gaa gag tat gtg gtc ctg aaa aac gag atg gca aga gca aac aat tat        693
Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn Asn Tyr
                185                     190                     195

aac gac tat ggg gat tat tgg aga ggg gac tat gaa gca gag gga gca        741
Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Ala Glu Gly Ala
                200                     205                     210

gat ggc tac aac tat aac cgt aac cag ttg att gaa gat gta gaa cgt        789
```

```
Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu Asp Val Glu Arg
        215                 220                 225
```

```
acc ttc gca gag atc aag cca ttg tat gag cat ctt cat gcc tat gtg        837
Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val
    230                 235                 240
```

```
agg agg aag ttg atg gat acc tac cct tcc tac atc agc ccc act gga        885
Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly
245                 250                 255                 260
```

```
tgc ctc cct gcc cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca        933

Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr
                265                 270                 275
```

```
aat ctg tac cct ttg act gtt ccc ttt gca cag aaa cca aac ata gat        981
Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys Pro Asn Ile Asp
                280                 285                 290
```

```
gtt act gat gca atg atg aat cag ggc tgg gat gca gaa agg ata ttt        1029
Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe
                295                 300                 305
```

```
caa gag gca gag aaa ttc ttt gtt tct gtt ggc ctt cct cat atg act        1077
Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu Pro His Met Thr
    310                 315                 320
```

```
caa gga ttc tgg gca aac tct atg ctg act gag cca gca gat ggc cgg        1125
Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg
325                 330                 335                 340
```

```
aaa gtt gtc tgc cac ccc aca gct tgg gat ctg gga cac gga gac ttc        1173
Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe
                345                 350                 355
```

```
aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc        1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala
                360                 365                 370
```

```
cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa        1269
```

His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln
        375   380   385

cct ttc ctg cta aga aac gga gcc aat gaa ggg ttc cat gaa gct gtt   1317
Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val
        390   395   400

gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc   1365
Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser
405   410   415   420

att ggt ctt ctg cca tcc gat ttt caa gaa gat agc gaa aca gag ata   1413
Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile
                425   430   435

aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt   1461

Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe
                440   445   450

act tac atg tta gag aag tgg agg tgg atg gtc ttt cgg ggt gaa att   1509
Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile
                455   460   465

ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc   1557
Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile
        470   475   480

gtt ggt gtg gtg gag cct ctg cct cgt gat gaa aca tac tgt gac cct   1605
Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr Tyr Cys Asp Pro
485   490   495   500

gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac   1653
Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr
                505   510   515

aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca   1701
Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala
                520   525   530

gct aag tat aat ggt tct ctg cac aaa tgt gac atc tca aat tcc act   1749

Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr
    535   540   545

gaa gct ggg cag aag ttg ctc aag atg ctg agt ctt gga aat tca gag   1797
Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu
    550   555   560

ccc tgg acc gaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat   1845
Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp
565   570   575   580

gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa   1893
Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys
           585   590   595

gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca   1941
Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro
        600   605   610

tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt   1989

Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu
      615   620   625

gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga   2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg
    630   635   640

tca tct gtt gca tat gcc atg aga aag tat tct tca ata atc aaa aac   2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser Ile Ile Lys Asn
645   650   655   660

cag aca gtt cct ttt cta gag gaa gat gta cga gtg agt gat ttg aaa   2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys
         665   670   675

cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct   2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser
        680   685   690

gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg   2229

```
Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg
    695                 700                 705
```

```
ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt      2277
Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe
    710                 715                 720
```

```
ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc      2325
Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr
725                 730                 735                 740
```

```
ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc      2373
Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly
                745                 750                 755
```

```
atc atc atc ctg att gtc act ggg atc aaa ggt cga aag aag aaa aat      2421
Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn
            760                 765                 770
```

```
gaa aca aaa aga gaa gag aac cct tat gac tcg atg gac att gga aaa      2469
Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys
        775                 780                 785
```

```
gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc      2517

Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser
    790                 795                 800
```

```
ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac           2570
Phe
805
```

```
acaaaatatg agagtataca catgtcatta gctatcaaaa ctatgatctg ttcagtaaac    2630
gttgtcca                                                             2638
```

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    <210> 9
    <211> 805
    <212> PRT
    <213> Mouse
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<400> 9

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr
1   5   10   15
Ala Gln Ser Leu Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe
            20   25   30
Asn Gln Glu Ala Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp
        35   40   45
Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu
        50   55   60
Ala Ala Ala Lys Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala
65   70   75   80
Gln Ser Phe Ser Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln
                85   90   95
Leu Gln Ala Leu Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys
            100   105   110
Asn Lys Gln Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
            115   120   125
Thr Gly Lys Val Cys Asn Pro Arg Asn Pro Gln Glu Cys Leu Leu Leu
        130   135   140
Glu Pro Gly Leu Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser
145   150   155   160
Arg Leu Trp Ala Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu
            165   170   175
Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
            180   185   190
Ala Asn Asn Tyr Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
            195   200   205
Ala Glu Gly Ala Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu
        210   215   220
Asp Val Glu Arg Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu
225   230   235   240
His Ala Tyr Val Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile
            245   250   255
Ser Pro Thr Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
            260   265   270
Arg Phe Trp Thr Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys
            275   280   285
Pro Asn Ile Asp Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala
        290   295   300
Glu Arg Ile Phe Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
305   310   315   320

Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro
               325   330   335

Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly
               340   345   350

His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn
               355   360   365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
               370   375   380

Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
385   390   395   400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
               405   410   415

His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser
               420   425   430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
             435   440   445

Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
        450   455   460

Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met
465   470   475   480

Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr
               485   490   495

Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
             500   505   510

Ile Arg Tyr Tyr Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala
             515   520   525

Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile
        530   535   540

Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu
545   550   555   560

Gly Asn Ser Glu Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala
             565   570   575

Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe
             580   585   590

Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr
             595   600   605

Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
        610   615   620

Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met
625   630   635   640

Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser
             645   650   655

```
Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val
            660                 665                 670
Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro
            675                 680                 685
Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile
        690                 695                 700
Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn
705                 710                 715                 720
Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln
                725                 730                 735
Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu
            740                 745                 750
Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg
            755                 760                 765
Lys Lys Lys Asn Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met
        770                 775                 780
Asp Ile Gly Lys Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp
785                 790                 795                 800
Ala Gln Thr Ser Phe
                805
```

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<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer.

<400> 10
gactccgatc atcaagcgtc aacta                                        25

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer.

<400> 11
ggcagggagg catccagtgg                                              20
```